

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/516,795
Source: PCT
Date Processed by STIC: 12-17-04

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 12/17/2004

PATENT APPLICATION: US/10/516,795

TIME: 15:49:32

Input Set : N:\FATIMA\10516795.txt

Output Set: N:\CRF4\12172004\J516795.raw

3 <110> APPLICANT: Susan M. Freier
 4 Brenda F. Baker
 5 Kenneth W. Dobie
 7 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF STEROL REGULATORY ELEMENT-BINDING
 PROTEIN-1
 8 EXPRESSION
 10 <130> FILE REFERENCE: ISIS0046-500
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/516,795
 C--> 12 <141> CURRENT FILING DATE: 2004-12-03
 12 <150> PRIOR APPLICATION NUMBER: US 10/161996
 14 <151> PRIOR FILING DATE: 2002-06-04
 16 <160> NUMBER OF SEQ ID NOS: 273
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 20
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Artificial Sequence
 24 <220> FEATURE:
 26 <223> OTHER INFORMATION: Antisense Oligonucleotide
 28 <400> SEQUENCE: 1
 29 tccgtcatcg ctctcaggg 20
 32 <210> SEQ ID NO: 2
 33 <211> LENGTH: 20
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Artificial Sequence
 37 <220> FEATURE:
 39 <223> OTHER INFORMATION: Antisense Oligonucleotide
 41 <400> SEQUENCE: 2
 42 gtgcgcgcga gcccgaaatc 20
 45 <210> SEQ ID NO: 3
 46 <211> LENGTH: 20
 47 <212> TYPE: DNA
 48 <213> ORGANISM: Artificial Sequence
 50 <220> FEATURE:
 52 <223> OTHER INFORMATION: Antisense Oligonucleotide
 54 <400> SEQUENCE: 3
 55 atgcattctg cccccaagga 20
 58 <210> SEQ ID NO: 4
 59 <211> LENGTH: 4154
 60 <212> TYPE: DNA
 61 <213> ORGANISM: H. sapiens
 63 <220> FEATURE:
 65 <221> NAME/KEY: CDS
 66 <222> LOCATION: (167)...(3610)
 68 <400> SEQUENCE: 4

(ps.6)

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69 taacgaggaa cttttcgccg gcgcccggcc gcctctgagg ccagggcagg acacgaacgc      60
71 gcggagcggc ggcggcgact gagagccggg gccgcggcgg cgctccctag gaagggccgt      120
73 acgagggcggc gggccccggcg ggcctcccgg aggagggcggc tgcgcc atg gac gag      175
74                                     Met Asp Glu
75                                     1
77 cca ccc ttc agc gag gcg gct ttg gag cag gcg ctg ggc gag ccg tgc      223
78 Pro Pro Phe Ser Glu Ala Ala Leu Glu Gln Ala Leu Gly Glu Pro Cys
79      5              10              15
81 gat ctg gac gcg gcg ctg ctg acc gac atc gaa gac atg ctt cag ctt      271
82 Asp Leu Asp Ala Ala Leu Leu Thr Asp Ile Glu Asp Met Leu Gln Leu
83 20              25              30              35
85 atc aac aac caa gac agt gac ttc cct ggc cta ttt gac cca ccc tat      319
86 Ile Asn Asn Gln Asp Ser Asp Phe Pro Gly Leu Phe Asp Pro Pro Tyr
87      40              45              50
89 gct ggg agt ggg gca ggg ggc aca gac cct gcc agc ccc gat acc agc      367
90 Ala Gly Ser Gly Ala Gly Gly Thr Asp Pro Ala Ser Pro Asp Thr Ser
91      55              60              65
93 tcc cca ggc agc ttg tct cca cct cct gcc aca ttg agc tcc tct ctt      415
94 Ser Pro Gly Ser Leu Ser Pro Pro Pro Ala Thr Leu Ser Ser Ser Leu
95      70              75              80
97 gaa gcc ttc ctg agc ggg ccg cag gca gcg ccc tca ccc ctg tcc cct      463
98 Glu Ala Phe Leu Ser Gly Pro Gln Ala Ala Pro Ser Pro Leu Ser Pro
99      85              90              95
101 ccc cag cct gca ccc act cca ttg aag atg tac ccg tcc atg ccc gct      511
102 Pro Gln Pro Ala Pro Thr Pro Leu Lys Met Tyr Pro Ser Met Pro Ala
103 100              105              110              115
105 ttc tcc cct ggg cct ggt atc aag gaa gag tca gtg cca ctg agc atc      559
106 Phe Ser Pro Gly Pro Gly Ile Lys Glu Glu Ser Val Pro Leu Ser Ile
107      120              125              130
109 ctg cag acc ccc acc cca cag ccc ctg cca ggg gcc ctc ctg cca cag      607
110 Leu Gln Thr Pro Thr Pro Gln Pro Leu Pro Gly Ala Leu Leu Pro Gln
111      135              140              145
113 agc ttc cca gcc cca gcc cca ccg cag ttc agc tcc acc cct gtg tta      655
114 Ser Phe Pro Ala Pro Ala Pro Pro Gln Phe Ser Ser Thr Pro Val Leu
115      150              155              160
117 ggc tac ccc agc cct ccg gga ggc ttc tct aca gga agc cct ccc ggg      703
118 Gly Tyr Pro Ser Pro Pro Gly Gly Phe Ser Thr Gly Ser Pro Pro Gly
119      165              170              175
121 aac acc cag cag ccg ctg cct ggc ctg cca ctg gct tcc ccg cca ggg      751
122 Asn Thr Gln Gln Pro Leu Pro Gly Leu Pro Leu Ala Ser Pro Pro Gly
123 180              185              190              195
125 gtc ccg ccc gtc tcc ttg cac acc cag gtc cag agt gtg gtc ccc cag      799
126 Val Pro Pro Val Ser Leu His Thr Gln Val Gln Ser Val Val Pro Gln
127      200              205              210
129 cag cta ctg aca gtc aca gct gcc ccc acg gca gcc cct gta acg acc      847
130 Gln Leu Leu Thr Val Thr Ala Ala Pro Thr Ala Ala Pro Val Thr Thr
131      215              220              225
133 act gtg acc tcg cag atc cag cag gtc ccg gtc ctg ctg cag ccc cac      895
134 Thr Val Thr Ser Gln Ile Gln Gln Val Pro Val Leu Leu Gln Pro His

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Input Set : N:\FATIMA\10516795.txt

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135	230	235	240	
137	ttc atc aag gca gac tcg ctg ctt ctg aca gcc atg aag aca gac gga	943		
138	Phe Ile Lys Ala Asp Ser Leu Leu Leu Thr Ala Met Lys Thr Asp Gly			
139	245 250 255			
141	gcc act gtg aag gcg gca ggt ctc agt ccc ctg gtc tct ggc acc act	991		
142	Ala Thr Val Lys Ala Ala Gly Leu Ser Pro Leu Val Ser Gly Thr Thr			
143	260 265 270 275			
145	gtg cag aca ggg cct ttg ccg acc ctg gtg agt ggc gga acc atc ttg	1039		
146	Val Gln Thr Gly Pro Leu Pro Thr Leu Val Ser Gly Gly Thr Ile Leu			
147	280 285 290			
149	gca aca gtc cca ctg gtc gta gat gcg gag aag ctg cct atc aac cgg	1087		
150	Ala Thr Val Pro Leu Val Val Asp Ala Glu Lys Leu Pro Ile Asn Arg			
151	295 300 305			
153	ctc gca gct ggc agc aag gcc ccg gcc tct gcc cag agc cgt gga gag	1135		
154	Leu Ala Ala Gly Ser Lys Ala Pro Ala Ser Ala Gln Ser Arg Gly Glu			
155	310 315 320			
157	aag cgc aca gcc cac aac gcc att gag aag cgc tac cgc tcc tcc atc	1183		
158	Lys Arg Thr Ala His Asn Ala Ile Glu Lys Arg Tyr Arg Ser Ser Ile			
159	325 330 335			
161	aat gac aaa atc att gag ctc aag gat ctg gtg gtg ggc act gag gca	1231		
162	Asn Asp Lys Ile Ile Glu Leu Lys Asp Leu Val Val Gly Thr Glu Ala			
163	340 345 350 355			
165	aag ctg aat aaa tct gct gtc ttg cgc aag gcc atc gac tac att cgc	1279		
166	Lys Leu Asn Lys Ser Ala Val Leu Arg Lys Ala Ile Asp Tyr Ile Arg			
167	360 365 370			
169	ttt ctg caa cac agc aac cag aaa ctc aag cag gag aac cta agt ctg	1327		
170	Phe Leu Gln His Ser Asn Gln Lys Leu Lys Gln Glu Asn Leu Ser Leu			
171	375 380 385			
173	cgc act gct gtc cac aaa agc aaa tct ctg aag gat ctg gtg tcg gcc	1375		
174	Arg Thr Ala Val His Lys Ser Lys Ser Leu Lys Asp Leu Val Ser Ala			
175	390 395 400			
177	tgt ggc agt gga ggg aac aca gac gtg ctc atg gag ggc gtg aag act	1423		
178	Cys Gly Ser Gly Gly Asn Thr Asp Val Leu Met Glu Gly Val Lys Thr			
179	405 410 415			
181	gag gtg gag gac aca ctg acc cca ccc ccc tcg gat gct ggc tca cct	1471		
182	Glu Val Glu Asp Thr Leu Thr Pro Pro Pro Ser Asp Ala Gly Ser Pro			
183	420 425 430 435			
185	ttc cag agc agc ccc ttg tcc ctt ggc agc agg ggc agt ggc agc ggt	1519		
186	Phe Gln Ser Ser Pro Leu Ser Leu Gly Ser Arg Gly Ser Gly Ser Gly			
187	440 445 450			
189	ggc agt ggc agt gac tcg gag cct gac agc cca gtc ttt gag gac agc	1567		
190	Gly Ser Gly Ser Asp Ser Glu Pro Asp Ser Pro Val Phe Glu Asp Ser			
191	455 460 465			
193	aag gca aag cca gag cag cgg ccg tct ctg cac agc cgg ggc atg ctg	1615		
194	Lys Ala Lys Pro Glu Gln Arg Pro Ser Leu His Ser Arg Gly Met Leu			
195	470 475 480			
197	gac cgc tcc cgc ctg gcc ctg tgc acg ctc gtc ttc ctc tgc ctg tcc	1663		
198	Asp Arg Ser Arg Leu Ala Leu Cys Thr Leu Val Phe Leu Cys Leu Ser			
199	485 490 495			

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201	tgc	aac	ccc	ttg	gcc	tcc	ttg	ctg	ggg	gcc	cgg	ggg	ctt	ccc	agc	ccc	1711
202	Cys	Asn	Pro	Leu	Ala	Ser	Leu	Leu	Gly	Ala	Arg	Gly	Leu	Pro	Ser	Pro	
203	500					505					510					515	
205	tca	gat	acc	acc	agc	gtc	tac	cat	agc	cct	ggg	cgc	aac	gtg	ctg	ggc	1759
206	Ser	Asp	Thr	Thr	Ser	Val	Tyr	His	Ser	Pro	Gly	Arg	Asn	Val	Leu	Gly	
207					520					525					530		
209	acc	gag	agc	aga	gat	ggc	cct	ggc	tgg	gcc	cag	tgg	ctg	ctg	ccc	cca	1807
210	Thr	Glu	Ser	Arg	Asp	Gly	Pro	Gly	Trp	Ala	Gln	Trp	Leu	Leu	Pro	Pro	
211				535					540					545			
213	gtg	gtc	tgg	ctg	ctc	aat	ggg	ctg	ttg	gtg	ctc	gtc	tcc	ttg	gtg	ctt	1855
214	Val	Val	Trp	Leu	Leu	Asn	Gly	Leu	Leu	Val	Leu	Val	Ser	Leu	Val	Leu	
215			550					555					560				
217	ctc	ttt	gtc	tac	ggt	gag	cca	gtc	aca	cgg	ccc	cac	tca	ggc	ccc	gcc	1903
218	Leu	Phe	Val	Tyr	Gly	Glu	Pro	Val	Thr	Arg	Pro	His	Ser	Gly	Pro	Ala	
219		565				570					575						
221	gtg	tac	ttc	tgg	agg	cat	cgc	aag	cag	gct	gac	ctg	gac	ctg	gcc	cgg	1951
222	Val	Tyr	Phe	Trp	Arg	His	Arg	Lys	Gln	Ala	Asp	Leu	Asp	Leu	Ala	Arg	
223	580					585					590					595	
225	gga	gac	ttt	gcc	cag	gct	gcc	cag	cag	ctg	tgg	ctg	gcc	ctg	cgg	gca	1999
226	Gly	Asp	Phe	Ala	Gln	Ala	Ala	Gln	Gln	Leu	Trp	Leu	Ala	Leu	Arg	Ala	
227				600					605					610			
229	ctg	ggc	cgg	ccc	ctg	ccc	acc	tcc	cac	ctg	gac	ctg	gct	tgt	agc	ctc	2047
230	Leu	Gly	Arg	Pro	Leu	Pro	Thr	Ser	His	Leu	Asp	Leu	Ala	Cys	Ser	Leu	
231				615					620					625			
233	ctc	tgg	aac	ctc	atc	cgt	cac	ctg	ctg	cag	cgt	ctc	tgg	gtg	ggc	cgc	2095
234	Leu	Trp	Asn	Leu	Ile	Arg	His	Leu	Leu	Gln	Arg	Leu	Trp	Val	Gly	Arg	
235			630						635					640			
237	tgg	ctg	gca	ggc	cgg	gca	ggg	ggc	ctg	cag	cag	gac	tgt	gct	ctg	cga	2143
238	Trp	Leu	Ala	Gly	Arg	Ala	Gly	Gly	Leu	Gln	Gln	Asp	Cys	Ala	Leu	Arg	
239		645				650					655						
241	gtg	gat	gct	agc	gcc	agc	gcc	cga	gac	gca	gcc	ctg	gtc	tac	cat	aag	2191
242	Val	Asp	Ala	Ser	Ala	Ser	Ala	Arg	Asp	Ala	Ala	Leu	Val	Tyr	His	Lys	
243	660					665					670					675	
245	ctg	cac	cag	ctg	cac	acc	atg	ggg	aag	cac	aca	ggc	ggg	cac	ctc	act	2239
246	Leu	His	Gln	Leu	His	Thr	Met	Gly	Lys	His	Thr	Gly	Gly	His	Leu	Thr	
247				680					685					690			
249	gcc	acc	aac	ctg	gcg	ctg	agt	gcc	ctg	aac	ctg	gca	gag	tgt	gca	ggg	2287
250	Ala	Thr	Asn	Leu	Ala	Leu	Ser	Ala	Leu	Asn	Leu	Ala	Glu	Cys	Ala	Gly	
251				695					700					705			
253	gat	gcc	gtg	tct	gtg	gcg	acg	ctg	gcc	gag	atc	tat	gtg	gcg	gct	gca	2335
254	Asp	Ala	Val	Ser	Val	Ala	Thr	Leu	Ala	Glu	Ile	Tyr	Val	Ala	Ala	Ala	
255			710						715					720			
257	ttg	aga	gtg	aag	acc	agt	ctc	cca	cgg	gcc	ttg	cat	ttt	ctg	aca	cgc	2383
258	Leu	Arg	Val	Lys	Thr	Ser	Leu	Pro	Arg	Ala	Leu	His	Phe	Leu	Thr	Arg	
259		725					730				735						
261	ttc	ttc	ctg	agc	agt	gcc	cgc	cag	gcc	tgc	ctg	gca	cag	agt	ggc	tca	2431
262	Phe	Phe	Leu	Ser	Ser	Ala	Arg	Gln	Ala	Cys	Leu	Ala	Gln	Ser	Gly	Ser	
263	740					745					750					755	
265	gtg	cct	cct	gcc	atg	cag	tgg	ctc	tgc	cac	ccc	gtg	ggc	cac	cgt	ttc	2479

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266	Val	Pro	Pro	Ala	Met	Gln	Trp	Leu	Cys	His	Pro	Val	Gly	His	Arg	Phe	
267					760					765					770		
269	ttc	gtg	gat	ggg	gac	tgg	tcc	gtg	ctc	agt	acc	cca	tgg	gag	agc	ctg	2527
270	Phe	Val	Asp	Gly	Asp	Trp	Ser	Val	Leu	Ser	Thr	Pro	Trp	Glu	Ser	Leu	
271				775					780					785			
273	tac	agc	ttg	gcc	ggg	aac	cca	gtg	gac	ccc	ctg	gcc	cag	gtg	act	cag	2575
274	Tyr	Ser	Leu	Ala	Gly	Asn	Pro	Val	Asp	Pro	Leu	Ala	Gln	Val	Thr	Gln	
275				790					795				800				
277	cta	ttc	cgg	gaa	cat	ctc	tta	gag	cga	gca	ctg	aac	tgt	gtg	acc	cag	2623
278	Leu	Phe	Arg	Glu	His	Leu	Leu	Glu	Arg	Ala	Leu	Asn	Cys	Val	Thr	Gln	
279				805					810				815				
281	ccc	aac	ccc	agc	cct	ggg	tca	gct	gat	ggg	gac	aag	gaa	ttc	tcg	gat	2671
282	Pro	Asn	Pro	Ser	Pro	Gly	Ser	Ala	Asp	Gly	Asp	Lys	Glu	Phe	Ser	Asp	
283	820					825						830				835	
285	gcc	ctc	ggg	tac	ctg	cag	ctg	ctg	aac	agc	tgt	tct	gat	gct	gcg	ggg	2719
286	Ala	Leu	Gly	Tyr	Leu	Gln	Leu	Leu	Asn	Ser	Cys	Ser	Asp	Ala	Ala	Gly	
287				840						845					850		
289	gct	cct	gcc	tac	agc	ttc	tcc	atc	agt	tcc	agc	atg	gcc	acc	acc	acc	2767
290	Ala	Pro	Ala	Tyr	Ser	Phe	Ser	Ile	Ser	Ser	Ser	Met	Ala	Thr	Thr	Thr	
291				855						860				865			
293	ggc	gta	gac	ccg	gtg	gcc	aag	tgg	tgg	gcc	tct	ctg	aca	gct	gtg	gtg	2815
294	Gly	Val	Asp	Pro	Val	Ala	Lys	Trp	Trp	Ala	Ser	Leu	Thr	Ala	Val	Val	
295				870					875				880				
297	atc	cac	tgg	ctg	cgg	cgg	gat	gag	gag	gcg	gct	gag	cgg	ctg	tgc	ccg	2863
298	Ile	His	Trp	Leu	Arg	Arg	Asp	Glu	Glu	Ala	Ala	Glu	Arg	Leu	Cys	Pro	
299				885					890				895				
301	ctg	gtg	gag	cac	ctg	ccc	cgg	gtg	ctg	cag	gag	tct	gag	aga	ccc	ctg	2911
302	Leu	Val	Glu	His	Leu	Pro	Arg	Val	Leu	Gln	Glu	Ser	Glu	Arg	Pro	Leu	
303	900					905						910				915	
305	ccc	agg	gca	gct	ctg	cac	tcc	ttc	aag	gct	gcc	cgg	gcc	ctg	ctg	ggc	2959
306	Pro	Arg	Ala	Ala	Leu	His	Ser	Phe	Lys	Ala	Ala	Arg	Ala	Leu	Leu	Gly	
307				920						925					930		
309	tgt	gcc	aag	gca	gag	tct	ggt	cca	gcc	agc	ctg	acc	atc	tgt	gag	aag	3007
310	Cys	Ala	Lys	Ala	Glu	Ser	Gly	Pro	Ala	Ser	Leu	Thr	Ile	Cys	Glu	Lys	
311				935					940					945			
313	gcc	agt	ggg	tac	ctg	cag	gac	agc	ctg	gct	acc	aca	cca	gcc	agc	agc	3055
314	Ala	Ser	Gly	Tyr	Leu	Gln	Asp	Ser	Leu	Ala	Thr	Thr	Pro	Ala	Ser	Ser	
315				950					955				960				
317	tcc	att	gac	aag	gcc	gtg	cag	ctg	ttc	ctg	tgt	gac	ctg	ctt	ctt	gtg	3103
318	Ser	Ile	Asp	Lys	Ala	Val	Gln	Leu	Phe	Leu	Cys	Asp	Leu	Leu	Leu	Val	
319				965					970				975				
321	gtg	cgc	acc	agc	ctg	tgg	cgg	cag	cag	cag	ccc	ccg	gcc	ccg	gcc	cca	3151
322	Val	Arg	Thr	Ser	Leu	Trp	Arg	Gln	Gln	Gln	Pro	Pro	Ala	Pro	Ala	Pro	
323	980					985						990				995	
325	gca	gcc	cag	ggc	gcc	agc	agc	agg	ccc	cag	gct	tcc	gcc	ctt	gag	ctg	3199
326	Ala	Ala	Gln	Gly	Ala	Ser	Ser	Arg	Pro	Gln	Ala	Ser	Ala	Leu	Glu	Leu	
327				1000						1005				1010			
329	cgt	ggc	ttc	caa	cgg	gac	ctg	agc	agc	ctg	agg	cgg	ctg	gca	cag	agc	3247
330	Arg	Gly	Phe	Gln	Arg	Asp	Leu	Ser	Ser	Leu	Arg	Arg	Leu	Ala	Gln	Ser	

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:99; N Pos. 352,415

Seq#:100; N Pos. 3861,3862,3863,3864,3865,3866,3867,3868,3869,3870,3871

Seq#:100; N Pos. 3872,3873,3874,3875,3876,3877,3878,3879,3880,3881,3882

Seq#:100; N Pos. 3883,3884,3885,3886,3887,3888,3889,3890,3891,3892,3893

Seq#:100; N Pos. 3894,3895,3896,3897,3898,3899,3900,3901,3902,3903,3904

Seq#:100; N Pos. 3905,3906,3907,3908,3909,3910,3911,3912,3913,3914,3915

Seq#:100; N Pos. 3916,3917,3918,3919,3920,3921,3922,3923,3924,3925,3926

Seq#:100; N Pos. 3927,3928,3929,3930,3931,3932,3933,3934,3935,3936,3937

Seq#:100; N Pos. 3938,3939,3940,3941,3942,3943,3944,3945,3946,3947,3948

Seq#:100; N Pos. 3949,3950,3951,3952,3953,3954,3955,3956,3957,3958,3959

Seq#:100; N Pos. 3960

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:3001 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:99,Line#:2997
L:3012 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:99 after pos.:300
M:341 Repeated in SeqNo=99
L:3161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:100 after pos.:3840
M:341 Repeated in SeqNo=100